

>at5g22330 1121D At5g22330 MIPS report.txt
Ruv DNA-helicase-like protein

General properties

Length [aa] 458
Molecular weight [Da] 50323.7
Isoelectric point 5.7
Manually edited no
Contig name chr5:chromosome5_v181103
Position [7449818] 7449818-7449729, 7449155-7448967,
7448846-7448715, 7448623-7448474, 7448267-7448112, 7447954-7447820, 7447734-7447669,
7447572-7447466, 7447374-7447275, 7447196-7447105, 7447022-7446953, 7446862-7446773
[7446773]
GC content [%] 43.7

Protein function

Closest homologue (BLASTP) TREMBL|AB007651.11 product: "Ruv DNA-helicase-like protein"; Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MWD9. 0.0

Functional categories 04 transcription
04.05 mrna transcription
04.05.01 mrna synthesis
04.05.01.01 general transcription activities
Automatically derived functional categories 63.03 nucleic acid binding 1e-137 -
H.sapiens_exp
40.10 nucleus 1e-137 - H.sapiens_exp
04 TRANSCRIPTION 1e-137 - H.sapiens_exp
03.01.05.03 DNA recombination 1e-137 - H.sapiens_exp
03.03.02 meiosis 1e-137 - H.sapiens_exp
25.05.25 gametogenesis 1e-137 - H.sapiens_exp
63.19 nucleotide binding 1e-137 - H.sapiens_put
63.01 protein binding 1e-134 - D.melanogaster_put
03.01.03 DNA synthesis and replication 1e-126 -
A.thaliana_put
03.01.05 DNA recombination and DNA repair 1e-126 -
A.thaliana_put
06.01 protein folding and stabilization 1e-123 -
H.sapiens_exp
40.03 cytoplasm 1e-123 - H.sapiens_exp
03.01.05.01 DNA repair 1e-123 - H.sapiens_exp
05 PROTEIN SYNTHESIS 1e-123 - H.sapiens_exp
62.01.07 binding / dissociation 1e-123 -
H.sapiens_exp
COGS
1e-62
COG1224 DNA helicase TIP49, TBP-interacting protein
PFAM domains
BLOCKS
COG0465 ATP-dependent Zn proteases 1e-39
PF06068 TIP49 C-terminus 1.5e-217
IPB001984 ATP-dependent serine proteases, Lon family
PR00819 CbxX/CfqX superfamily signature
PR00918 Calicivirus non-structural polyprotein
family signature
IPB002648 Isopentenyl transferase
IPB003442 Uncharacterised P-loop hydrolase UPF0079
PROSITE motifs
ATP_GTP_A (1)

Automatically derived PIR superfamilies PIR|JC5521 JC5135 0.0
PIR|JC5521 trehalose trehalohydrolase 0.0
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PIR|JE0334 hydrolase 0.0

PIR|T19534 n MJ1163 1e-135

PIR|T40697 ein MJ1163 2e-97

PIR|F75150 63 5e-96

PIR|S61029 se 1e-94

PIR|D71191 RY ah1827 1e-94

PIR|T46049 conserved hypothetical protein MJ1163

2e-93

Automatically derived keywords

PIR|D69476 se trehalohydrolase 2e-90

PIR|JC5521 atp 0.0

Protein structure

Known3D

Subunit Gamma

PDB|lnjg mol:protein length:250 DNA Polymerase III

Metalloprotease Ftsh

PDB|l1xz mol:protein length:254 ATP-Dependent

N-Ethylmaleimide-Sensitive Fusion Protein

PDB|llv7 mol:protein length:257 Ftsh

PDB|ldzn mol:protein length:272

Sensitive Factor

PDB|lnsf mol:protein length:273 N-Ethylmaleimide

Metalloprotease Ftsh

PDB|liy2 mol:protein length:278 ATP-Dependent

Protease ATP-Binding Subun

PDB|lofh mol:protein length:310 ATP-Dependent Hsl

DNA Helicase Ruvb

PDB|lhqc mol:protein length:324 Ruvb

PDB|liqp mol:protein length:327 Rfcs

PDB|lin5 mol:protein length:334 Holliday Junction

Subunit Gamma

PDB|ljr3 mol:protein length:373 DNA Polymerase III

Protease ATP-Binding Subun

PDB|ldo0 mol:protein length:442 Heat Shock Locus U

PDB|lg4a mol:protein length:443 ATP-Dependent Hsl

Protease ATP-Binding Subun

PDB|lkyi mol:protein length:444 ATP-Dependent Hsl

Protease ATP-Binding Subu

PDB|lg3i mol:protein length:444 ATP-Dependent Hslu

Hslu

PDB|lg41 mol:protein length:444 Heat Shock Protein

Protease ATP-Binding Subun

PDB|le32 mol:protein length:458 P97

PDB|lksf mol:protein length:758 ATP-Dependent Clp

Endoplasmic Reticulum Atpase

PDB|loz4 mol:protein length:806 Transitional

Hsl Protease ATP-Binding S

PDB|lqvr mol:protein length:854 Clpb Protein

PDB|lim2 mol:protein-het length:444 ATP-Dependent

SCOP domains

N-ethylmaleimide-sensitive fusion (NSF) protein {Chinese hamster (Cricetulus griseus)}

dld2na_ c.37.1.13 (A:) Hexamerization domain of

helicase RuvB {Thermotoga maritima}

dlg41a_ c.37.1.13 (A:) Hslu {Haemophilus influenzae}

dlin4a2 c.37.1.13 (A:17-254) Holliday junction

{Archaeon Pyrococcus furiosus}

dliqpa2 c.37.1.13 (A:2-232) Replication factor C

p97, D1 domain {Mouse (Mus musculus)}

dle32a2 c.37.1.13 (A:201-458) Membrane fusion atpase

Structural class

Alpha_Beta

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